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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/927,565

DATE: 01/15/2002
 TIME: 09:58:29

Input Set : N:\Crif3\RULE60\09927565.raw
 Output Set: N:\CRF3\01152002\I927565.raw

#2.

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: Lal, Preeti
 6 Shah, Purvi
 7 Corley, Neil C.
 9 (ii) TITLE OF INVENTION: HUMAN PREPRONEUROTENSIN/NEUROMEDIN N
 11 (iii) NUMBER OF SEQUENCES: 4
 13 (iv) CORRESPONDENCE ADDRESS:
 14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 15 (B) STREET: 3174 Porter Drive
 16 (C) CITY: Palo Alto
 17 (D) STATE: CA
 18 (E) COUNTRY: USA
 19 (F) ZIP: 94304
 21 (v) COMPUTER READABLE FORM:
 22 (A) MEDIUM TYPE: Diskette
 23 (B) COMPUTER: IBM Compatible
 24 (C) OPERATING SYSTEM: DOS
 25 (D) SOFTWARE: FastSEQ for Windows Version 2.0
 27 (vi) CURRENT APPLICATION DATA:
 C--> 28 (A) APPLICATION NUMBER: US/09/927,565
 C--> 29 (B) FILING DATE: 09-Aug-2001
 30 (C) CLASSIFICATION:
 32 (vii) PRIOR APPLICATION DATA:
 33 (A) APPLICATION NUMBER: 09/002,114
 34 (B) FILING DATE:
 36 (viii) ATTORNEY/AGENT INFORMATION:
 37 (A) NAME: Billings, Lucy J.
 38 (B) REGISTRATION NUMBER: 36,749
 39 (C) REFERENCE/DOCKET NUMBER: PF-0450 US
 41 (ix) TELECOMMUNICATION INFORMATION:
 42 (A) TELEPHONE: 650-855-0555
 43 (B) TELEFAX: 650-845-4166
 44 (C) TELEX:
 47 (2) INFORMATION FOR SEQ ID NO: 1:
 49 (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 170 amino acids
 51 (B) TYPE: amino acid
 52 (C) STRANDEDNESS: single
 53 (D) TOPOLOGY: linear
 55 (vii) IMMEDIATE SOURCE:
 56 (A) LIBRARY: PITUNOT03
 57 (B) CLONE: 1760566
 59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 61 Met Met Ala Gly Met Lys Ile Gln Leu Val Cys Met Leu Leu Leu Ala
 62 1 5 10 15
 63 Phe Ser Ser Trp Ser Leu Cys Ser Asp Ser Glu Glu Glu Met Lys Ala

ENTERED

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64          20          25          30
65 Leu Glu Ala Asp Phe Leu Thr Asn Met His Thr Ser Lys Ile Ser Lys
66          35          40          45
67 Ala His Val Pro Ser Trp Lys Met Thr Leu Leu Asn Val Cys Ser Leu
68          50          55          60
69 Val Asn Asn Leu Asn Ser Pro Ala Glu Glu Thr Gly Glu Val His Glu
70 65          70          75          80
71 Glu Glu Leu Val Ala Arg Arg Lys Leu Pro Thr Ala Leu Asp Gly Phe
72          85          90          95
73 Ser Leu Glu Ala Met Leu Thr Ile Tyr Gln Leu His Lys Ile Cys His
74          100          105          110
75 Ser Arg Ala Phe Gln His Trp Glu Leu Ile Gln Glu Asp Ile Leu Asp
76          115          120          125
77 Thr Gly Asn Asp Lys Asn Gly Lys Glu Glu Val Ile Lys Arg Lys Ile
78          130          135          140
79 Pro Tyr Ile Leu Lys Arg Gln Leu Tyr Glu Asn Lys Pro Arg Arg Pro
80 145          150          155          160
81 Tyr Ile Leu Lys Arg Asp Ser Tyr Tyr Tyr
82          165          170

```

84 (2) INFORMATION FOR SEQ ID NO: 2:

86 (i) SEQUENCE CHARACTERISTICS:

87 (A) LENGTH: 1351 base pairs

88 (B) TYPE: nucleic acid

89 (C) STRANDEDNESS: single

90 (D) TOPOLOGY: linear

93 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

95 NNTCAAAGCC AGCTGAAGGA AAGAGGAAGT GCTAGAGAGA GCCCCCTTCA GTGTGCTTCT      60
96 GACTTTTACG GACTTGGCTT GTTAGAAGGC TGAAAGATGA TGGCAGGAAT GAAAATCCAG      120
97 CTTGTATGCA TGCTACTCCT GGCTTTCAGC TCCTGGAGTC TGTGCTCAGA TTCAGAAGAG      180
98 GAAATGAAAG CATTAGAAGC AGATTTCTTG ACCAATATGC ATACATCAAA GATTAGTAAA      240
99 GCACATGTTT CCTCTTGGA GATGACTCTG CTAAATGTTT GCAGTCTTGT AAATAATTTG      300
100 AACAGCCCAG CTGAGGAAAC AGGAGAAGTT CATGAAGAGG AGCTTGTTGC AAGAAGGAAA      360
101 CTTCCTACTG CTTTAGATGG CTTTAGCTTG GAAGCAATGT TGACAATATA CCAGCTCCAC      420
102 AAAATCTGTC ACAGCAGGGC TTTTCAACAC TGGGAGTTAA TCCAGGAAGA TATTCTTGAT      480
103 ACTGGAAATG ACAAAAATGG AAAGGAAGAA GTCATAAAGA GAAAAATTCC TTATATTCTG      540
104 AAACGGCAGC TGTATGAGAA TAAACCCAGA AGACCCTACA TACTCAAAAG AGATTCTTAC      600
105 TATTACTGAG AGAATAAATC ATTTATTTAC ATGTGATTGT GATTCATCAT CCCTTAATTA      660
106 AATATCAAAT TATATTTGTG TGAAAATGTG ACAAACACAC TTATCTGTCT CTTCTACAAT      720
107 TGTGGTTTAT TGAATGTGAT TTTTCTGCAC TAATATAAAT TAGACTAAGT GTTTTCAAAT      780
108 AAATCTAAAT CTTCAGCATG ATGTGTTGTG TATAATTGGA GTAGATATTA ATTAAGTCAC      840
109 CTGTATAATG TTTTGTAATT TTGCAAAACA TATCTTGAGT TGTTTAAACA GTCAAAATGT      900
110 TTGATATTTT ATACCAGCTT ATGAGCTCAA AGTACTACAG CAAAGCCTAG CCTGCATATC      960
111 ATTCACCCAA AACAAAGTAA TAGCGCCTCT TTTATTATTT TGACTGAATG TTTTATGGAA      1020
112 TTGAAAGAAA CATACGTTCT TTTCAAGACT TCCTCATGAA TCTCTCAATT ATAGGAAAAG      1080
113 TTATTGTGAT AAAATAGGAA CAGCTGAAAG ATTGATTAAT GAACATTGT TATTACTTCC      1140
114 TATTTTAATG AATGACATTG AACTGGATTT TTTGACCTGT TAATGGACTT GGTAGCTATT      1200
115 AGAAGGACAC TTGACCTCCA ATAGAAAAAA AATAAAGAAA TAAAAAGAAG TATAAAAGTA      1260
116 ATAAAATAAA ATCAGAAGAG AAAAAGAAAA AGAAAAGTAA AAAGAGGGGG GACACACCAT      1320
117 AAGAACCAAT ACCCGGGAAT TTTCGGAGCG A                                1351

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120 (2) INFORMATION FOR SEQ ID NO: 3:

122 (i) SEQUENCE CHARACTERISTICS:

123 (A) LENGTH: 169 amino acids

124 (B) TYPE: amino acid

125 (C) STRANDEDNESS: single

126 (D) TOPOLOGY: linear

128 (vii) IMMEDIATE SOURCE:

129 (A) LIBRARY: GenBank

130 (B) CLONE: 163424

132 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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134 Met Ala Gly Met Lys Ile Gln Leu Val Cys Met Ile Leu Leu Ala Phe
135 1 5 10 15
136 Ser Ser Trp Ser Leu Cys Ser Asp Ser Glu Glu Glu Met Lys Ala Leu
137 20 25 30
138 Glu Thr Asp Leu Leu Thr Asn Met His Thr Ser Lys Ile Ser Lys Ala
139 35 40 45
140 Ser Val Pro Ser Trp Lys Met Ser Leu Leu Asn Val Cys Ser Leu Ile
141 50 55 60
142 Asn Asn Leu Asn Ser Gln Ala Glu Glu Thr Gly Glu Phe His Glu Glu
143 65 70 75 80
144 Glu Leu Ile Thr Arg Arg Lys Phe Pro Ala Ala Leu Asp Gly Phe Ser
145 85 90 95
146 Leu Glu Ala Met Leu Thr Ile Tyr Gln Leu Gln Lys Ile Cys His Ser
147 100 105 110
148 Arg Ala Phe Gln His Trp Glu Leu Ile Gln Glu Asp Ile Leu Asp Ala
149 115 120 125
150 Gly Asn Asp Lys Asn Glu Lys Glu Glu Val Ile Lys Arg Lys Ile Pro
151 130 135 140
152 Tyr Ile Leu Lys Arg Gln Leu Tyr Glu Asn Lys Pro Arg Arg Pro Tyr
153 145 150 155 160
154 Ile Leu Lys Arg Gly Ser Tyr Tyr Tyr
155 165

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157 (2) INFORMATION FOR SEQ ID NO: 4:

159 (i) SEQUENCE CHARACTERISTICS:

160 (A) LENGTH: 169 amino acids

161 (B) TYPE: amino acid

162 (C) STRANDEDNESS: single

163 (D) TOPOLOGY: linear

165 (vii) IMMEDIATE SOURCE:

166 (A) LIBRARY: GenBank

167 (B) CLONE: 92546

169 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

171 Met Ile Gly Met Asn Leu Gln Leu Val Cys Leu Thr Leu Leu Ala Phe
172 1 5 10 15
173 Ser Ser Trp Ser Leu Cys Ser Asp Ser Glu Glu Asp Val Arg Ala Leu
174 20 25 30
175 Glu Ala Asp Leu Leu Thr Asn Met His Ala Ser Lys Val Ser Lys Gly
176 35 40 45
177 Ser Pro Pro Ser Trp Lys Met Thr Leu Leu Asn Val Cys Ser Leu Ile

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```

178      50      55      60
179 Asn Asn Leu Asn Ser Ala Ala Glu Glu Ala Gly Glu Met Arg Asp Asp
180 65      70      75      80
181 Asp Leu Val Ala Lys Arg Lys Leu Pro Leu Val Leu Asp Asp Phe Ser
182      85      90      95
183 Leu Glu Ala Leu Leu Thr Val Phe Gln Leu Gln Lys Ile Cys Arg Ser
184      100     105     110
185 Arg Ala Phe Gln His Trp Glu Ile Ile Gln Glu Asp Ile Leu Asp His
186      115     120     125
187 Gly Asn Glu Lys Thr Glu Lys Glu Glu Val Ile Lys Arg Lys Ile Pro
188      130     135     140
189 Tyr Ile Leu Lys Arg Gln Leu Tyr Glu Asn Lys Pro Arg Arg Pro Tyr
190 145     150     155     160
191 Ile Leu Lys Arg Ala Ser Tyr Tyr Tyr
192      165

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VERIFICATION SUMMARY

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]